

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga  
 Hillman, Jennifer L.  
 Corley, Neil C.  
 Guegler, Karl G.  
 Lal, Preeti  
 Goli, Surya K.  
 Shah, Purvi

(ii) TITLE OF THE INVENTION: DISEASE ASSOCIATED PROTEIN KINASES

(iii) NUMBER OF SEQUENCES: 21

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 (B) STREET: 3174 Porter Drive  
 (C) CITY: Palo Alto  
 (D) STATE: CA  
 (E) COUNTRY: USA  
 (F) ZIP: 94304

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette  
 (B) COMPUTER: IBM Compatible  
 (C) OPERATING SYSTEM: DOS  
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned  
 (B) FILING DATE: Filed Herewith

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:  
 (B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.  
 (B) REGISTRATION NUMBER: 36,749  
 (C) REFERENCE/DOCKET NUMBER: PF-0321 US

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555  
 (B) TELEFAX: 415-845-4166

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01  
 (B) CLONE: 39043

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
 1                               5                               10                               15
Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
                               20                               25                               30
Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln

```

35										40										45														
Ala	Gln	Val	Pro	Pro	Ala	Ala	Pro	His	His	His	His	His	His	Ser	His	Ala	Pro	His	His	His	His	His	His	Ser	His	Ala	Pro	His	His	His	His	Ser	His	
50						55										60										65								
Ser	Gly	Pro	Glu	Ile	Ser	Arg	Ile	Ile	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ser	Arg	Ile	Ile	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ser	Arg	Ile	Ile	Val	Asp	Pro	Thr
65					70											75										80								
Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu	Gly	Lys	Gly	Gly	Phe	Ala	Lys	Cys	Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu	Gly	Lys	Cys	Arg	Tyr	Cys	Arg	Gly	Lys	Val	Leu
				85												90										95								
Tyr	Glu	Met	Thr	Asp	Leu	Thr	Asn	Asn	Lys	Val	Tyr	Ala	Ala	Lys	Ile	Tyr	Glu	Met	Thr	Asp	Leu	Thr	Asn	Asn	Lys	Val	Tyr	Ala	Ala	Lys	Ile			
			100													105										110								
Ile	Pro	His	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys	Ile	Asp	Ile	Pro	His	Ser	Arg	Val	Ala	Lys	Pro	His	Gln	Arg	Glu	Lys	Ile	Asp			
			115													120										125								
Lys	Glu	Ile	Glu	Leu	His	Arg	Ile	Leu	His	His	Lys	His	Val	Val	Gln	Lys	Glu	Ile	Glu	Leu	His	Arg	Ile	Leu	His	His	Lys	His	Val	Val	Gln			
			130			135										140										145								
Phe	Tyr	His	Tyr	Phe	Glu	Asp	Lys	Glu	Asn	Ile	Tyr	Ile	Leu	Leu	Glu	Phe	Tyr	His	Tyr	Phe	Glu	Asp	Lys	Glu	Asn	Ile	Tyr	Ile	Leu	Leu	Glu			
145					150											155										160								
Tyr	Cys	Ser	Arg	Arg	Ser	Met	Ala	His	Ile	Leu	Lys	Ala	Arg	Lys	Val	Tyr	Cys	Ser	Arg	Arg	Ser	Met	Ala	His	Ile	Leu	Lys	Ala	Arg	Lys	Val			
				165												170										175								
Leu	Thr	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Val	Ser	Gly	Leu	Thr	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg	Gln	Ile	Val	Ser	Gly			
			180													185										190								
Leu	Lys	Tyr	Leu	His	Glu	Gln	Glu	Ile	Leu	His	Arg	Asp	Leu	Lys	Leu	Leu	Lys	Tyr	Leu	His	Glu	Gln	Glu	Ile	Leu	His	Arg	Asp	Leu	Lys	Leu			
			195													200										205								
Gly	Asn	Phe	Phe	Ile	Asn	Glu	Ala	Met	Glu	Leu	Lys	Val	Gly	Asp	Phe	Gly	Asn	Phe	Phe	Ile	Asn	Glu	Ala	Met	Glu	Leu	Lys	Val	Gly	Asp	Phe			
			210													215										220								
Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Leu	Glu	His	Arg	Arg	Arg	Thr	Ile	Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Leu	Glu	His	Arg	Arg	Arg	Thr	Ile			
225					230											235										240								
Cys	Gly	Thr	Pro	Asn	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Asn	Lys	Gln	Gly	Cys	Gly	Thr	Pro	Asn	Tyr	Leu	Ser	Pro	Glu	Val	Leu	Asn	Lys	Gln	Gly			
				245												250										255								
His	Gly	Cys	Glu	Ser	Asp	Ile	Trp	Ala	Leu	Gly	Cys	Val	Met	Tyr	Thr	His	Gly	Cys	Glu	Ser	Asp	Ile	Trp	Ala	Leu	Gly	Cys	Val	Met	Tyr	Thr			
			260													265										270								
Met	Leu	Leu	Gly	Arg	Pro	Pro	Phe	Glu	Thr	Thr	Asn	Leu	Lys	Glu	Thr	Met	Leu	Leu	Gly	Arg	Pro	Pro	Phe	Glu	Thr	Thr	Asn	Leu	Lys	Glu	Thr			
			275													280										285								
Tyr	Arg	Cys	Ile	Arg	Glu	Ala	Arg	Tyr	Thr	Met	Pro	Ser	Ser	Leu	Leu	Tyr	Arg	Cys	Ile	Arg	Glu	Ala	Arg	Tyr	Thr	Met	Pro	Ser	Ser	Leu	Leu			
			290													295										300								
Ala	Pro	Ala	Lys	His	Leu	Ile	Ala	Ser	Met	Leu	Ser	Lys	Asn	Pro	Glu	Ala	Pro	Ala	Lys	His	Leu	Ile	Ala	Ser	Met	Leu	Ser	Lys	Asn	Pro	Glu			
305					310											315										320								
Asp	Arg	Pro	Ser	Leu	Asp	Asp	Ile	Ile	Arg	His	Asp	Phe	Phe	Leu	Gln	Asp	Arg	Pro	Ser	Leu	Asp	Asp	Ile	Ile	Arg	His	Asp	Phe	Phe	Leu	Gln			
				325												330										335								
Gly	Phe	Thr	Pro	Asp	Arg	Leu	Ser	Ser	Ser	Cys	Cys	His	Thr	Val	Pro	Gly	Phe	Thr	Pro	Asp	Arg	Leu	Ser	Ser	Ser	Cys	Cys	His	Thr	Val	Pro			
			340													345										350								
Asp	Phe	His	Leu	Ser	Ser	Pro	Ala	Lys	Asn	Phe	Phe	Lys	Lys	Ala	Ala	Asp	Phe	His	Leu	Ser	Ser	Pro	Ala	Lys	Asn	Phe	Phe	Lys	Lys	Ala	Ala			
			355													360										365								
Ala	Ala	Leu	Phe	Gly	Gly	Lys	Lys	Asp	Lys	Ala	Arg	Tyr	Ile	Asp	Thr	Ala	Ala	Leu	Phe	Gly	Gly	Lys	Lys	Asp	Lys	Ala	Arg	Tyr	Ile	Asp	Thr			
			370													375										380								
His	Asn	Arg	Val	Ser	Lys	Glu	Asp	Glu	Asp	Ile	Tyr	Lys	Leu	Arg	His	His	Asn	Arg	Val	Ser	Lys	Glu	Asp	Glu	Asp	Ile	Tyr	Lys	Leu	Arg	His			
385					390											395										400								
Asp	Leu	Lys	Lys	Thr	Ser	Ile	Thr	Gln	Gln	Pro	Ser	Lys	His	Arg	Thr	Asp	Leu	Lys	Lys	Thr	Ser	Ile	Thr	Gln	Gln	Pro	Ser	Lys	His	Arg	Thr			
				405												410										415								
Asp	Glu	Glu	Leu	Gln	Pro	Pro	Thr	Thr	Thr	Val	Ala	Arg	Ser	Gly	Thr	Asp	Glu	Glu	Leu	Gln	Pro	Pro	Thr	Thr	Thr	Val	Ala	Arg	Ser	Gly	Thr			
			420													425										430								

```

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
      435
Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
      450
Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
      465
Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
      485
Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
      500
Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
      515
Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Ala
      530
His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
      545
Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
      565
His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
      580
Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Gln Trp Leu Lys Ser
      595
Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
      610
Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu
      625
Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
      645
Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
      660
Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
      675
      680
      685

```

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYNOT01
- (B) CLONE: 40194

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Pro Pro Lys Arg Asn Glu Lys Tyr Lys Leu Pro Ile Pro Phe Pro
1      5      10      15
Glu Gly Lys Val Leu Asp Asp Met Glu Gly Asn Gln Trp Val Leu Gly
20      25      30
Lys Lys Ile Gly Ser Gly Gly Phe Gly Leu Ile Tyr Leu Ala Phe Pro
35      40      45
Thr Asn Lys Pro Glu Lys Asp Ala Arg His Val Val Lys Val Glu Tyr
50      55      60
Gln Glu Asn Gly Pro Leu Phe Ser Glu Leu Lys Phe Tyr Gln Arg Val
65      70      75      80
Ala Lys Lys Asp Cys Ile Lys Lys Trp Ile Glu Arg Lys Gln Leu Asp
85      90      95
Tyr Leu Gly Ile Pro Leu Phe Tyr Gly Ser Gly Leu Thr Glu Phe Lys
100      105      110
Gly Arg Ser Tyr Arg Phe Met Val Met Glu Arg Leu Gly Ile Asp Leu
115      120      125
Gln Lys Ile Ser Gly Gln Asn Gly Thr Phe Lys Lys Ser Thr Val Leu
130      135      140

```

Gln	Leu	Gly	Ile	Arg	Met	Leu	Asp	Val	Leu	Glu	Tyr	Ile	His	Glu	Asn	145	150	155	160
Glu	Tyr	Val	His	Gly	Asp	Val	Lys	Ala	Ala	Asn	Leu	Leu	Leu	Gly	Tyr	165	170	175	
Lys	Asn	Pro	Asp	Gln	Val	Tyr	Leu	Ala	Asp	Tyr	Gly	Leu	Ser	Tyr	Arg	180	185	190	
Tyr	Cys	Pro	Asn	Gly	Asn	His	Lys	Gln	Tyr	Gln	Glu	Asn	Pro	Arg	Lys	195	200	205	
Gly	His	Asn	Gly	Thr	Ile	Glu	Phe	Thr	Ser	Leu	Asp	Ala	His	Lys	Gly	210	215	220	
Val	Gly	Glu	Ile	Ala	Gln	Phe	Leu	Val	Cys	Ala	His	Ser	Leu	Ala	Tyr	225	230	235	
Asp	Glu	Lys	Pro	Asn	Tyr	Gln	Ala	Leu	Lys	Lys	Ile	Leu	Asn	Pro	His	245	250	255	
Gly	Ile	Pro	Leu	Gly	Pro	Leu	Asp	Phe	Ser	Thr	Lys	Gly	Gln	Ser	Ile	260	265	270	
Asn	Val	His	Thr	Pro	Asn	Ser	Gln	Lys	Val	Asp	Ser	Gln	Lys	Ala	Ala	275	280	285	
Thr	Lys	Gln	Val	Asn	Lys	Ala	His	Asn	Arg	Leu	Ile	Glu	Lys	Lys	Val	290	295	300	
His	Ser	Glu	Arg	Ser	Ala	Glu	Ser	Cys	Ala	Thr	Trp	Lys	Val	Gln	Lys	305	310	315	
Glu	Glu	Lys	Leu	Ile	Gly	Leu	Met	Asn	Asn	Glu	Ala	Ala	Gln	Glu	Ser	325	330	335	
Thr	Arg	Arg	Arg	Gln	Lys	Tyr	Gln	Glu	Ser	Gln	Glu	Pro	Leu	Asn	Glu	340	345	350	
Val	Asn	Ser	Phe	Pro	Gln	Lys	Ile	Ser	Tyr	Thr	Gln	Phe	Pro	Asn	Ser	355	360	365	
Phe	Tyr	Glu	Pro	His	Gln	Asp	Phe	Thr	Ser	Pro	Asp	Ile	Phe	Lys	Lys	370	375	380	
Ser	Arg	Ser	Pro	Ser	Trp	Tyr	Lys	Tyr	Thr	Ser	Thr	Val	Ser	Thr	Gly	385	390	395	
Ile	Thr	Asp	Leu	Glu	Ser	Ser	Thr	Gly	Leu	Trp	Pro	Thr	Ile	Ser	Gln	405	410	415	
Phe	Thr	Leu	Ser	Glu	Glu	Thr	Asn	Ala	Asp	Val	Tyr	Tyr	Tyr	Arg	Ile	420	425	430	
Ile	Ile	Pro	Val	Leu	Leu	Met	Leu	Val	Phe	Leu	Ala	Leu	Phe	Phe	Leu	435	440	445	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01
- (B) CLONE: 402339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	Ala	Arg	Arg	Lys	Pro	Val	Leu	Pro	Ala	Leu	Thr	Ile	Asn	Pro	1	5	10	15
Thr	Ile	Ala	Glu	Gly	Pro	Ser	Pro	Thr	Ser	Glu	Gly	Ala	Ser	Glu	Ala	20	25	30	
Asn	Leu	Val	Asp	Leu	Gln	Lys	Lys	Leu	Glu	Glu	Leu	Glu	Leu	Asp	Glu	35	40	45	
Gln	Gln	Lys	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys	Val	50	55	60	
Gly	Glu	Leu	Lys	Asp	Asp	Asp	Phe	Glu	Arg	Ile	Ser	Glu	Leu	Gly	Ala	65	70	75	
Gly	Asn	Gly	Gly	Val	Val	Thr	Lys	Val	Gln	His	Arg	Pro	Ser	Gly	Leu	85	90	95	

```

Ile Met Ala Arg Lys Leu Ile His Leu Glu Ile Lys Pro Ala Ile Arg
      100      105      110
Asn Gln Ile Ile Arg Glu Leu Gln Val Leu His Glu Cys Asn Ser Pro
      115      120      125
Tyr Ile Val Gly Phe Tyr Gly Ala Phe Tyr Ser Asp Gly Glu Ile Ser
      130      135      140
Ile Cys Met Glu His Met Asp Gly Gly Ser Leu Asp His Leu Leu Lys
      145      150      155      160
Glu Ala Lys Arg Ile Pro Glu Glu Ile Leu Gly Lys Val Ser Ile Ala
      165      170      175
Val Leu Arg Gly Leu Ala Tyr Leu Arg Glu Lys His Gln Ile Met His
      180      185      190
Arg Asp Val Lys Pro Ser Asn Ile Leu Val Asn Ser Arg Gly Glu Ile
      195      200      205
Lys Leu Cys Asp Phe Gly Val Ser Gly Gln Leu Ile Asp Ser Met Ala
      210      215      220
Asn Ser Phe Val Gly Thr Arg Ser Tyr Met Ala Pro Glu Arg Leu Gln
      225      230      235      240
Gly Thr His Tyr Ser Val Gln Ser Asp Ile Trp Ser Met Gly Leu Ser
      245      250      255
Leu Val Glu Leu Ala Val Gly Arg Tyr Pro Ile Pro Pro Pro Asp Ala
      260      265      270
Lys Glu Leu Glu Ala Ile Phe Gly Arg Pro Val Val Asp Gly Glu Glu
      275      280      285
Gly Glu Pro His Ser Ile Ser Pro Arg Pro Arg Pro Pro Gly Arg Pro
      290      295      300
Val Ser Gly His Gly Met Asp Ser Arg Pro Ala Met Ala Ile Phe Glu
      305      310      315      320
Leu Leu Asp Tyr Ile Val Asn Glu Pro Pro Pro Lys Leu Pro Asn Gly
      325      330      335
Val Phe Thr Pro Asp Phe Gln Glu Phe Val Asn Lys Cys Leu Ile Lys
      340      345      350
Asn Pro Ala Glu Arg Ala Asp Leu Lys Met Leu Thr Asn His Thr Phe
      355      360      365
Ile Lys Arg Ser Glu Val Glu Glu Val Asp Phe Ala Gly Trp Leu Cys
      370      375      380
Lys Thr Leu Arg Leu Asn Gln Pro Gly Thr Pro Thr Arg Thr Ala Val
      385      390      395      400

```

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04
- (B) CLONE: 705365

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Met Ala Met Thr Ala Gly Thr Thr Thr Thr Phe Pro Met Ser Asn His
  1      5      10
Thr Arg Glu Arg Val Thr Val Ala Lys Leu Thr Leu Glu Asn Phe Tyr
      20      25      30
Ser Asn Leu Ile Leu Gln His Glu Glu Arg Glu Thr Arg Gln Lys Lys
      35      40      45
Leu Glu Val Ala Met Glu Glu Glu Gly Leu Ala Asp Glu Glu Lys Lys
      50      55      60
Leu Arg Arg Ser Gln His Ala Arg Lys Glu Thr Glu Phe Leu Arg Leu
      65      70      75      80
Lys Arg Thr Arg Leu Gly Leu Asp Asp Phe Glu Ser Leu Lys Val Ile
      85      90      95
Gly Arg Gly Ala Phe Gly Glu Val Arg Leu Val His Lys Lys Asp Thr

```

100										105					110				
Gly	His	Ile	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Ser	Asp	Met	Leu	Glu				
Lys	Glu	Gln	Val	Ala	His	Ile	Arg	Ala	Glu	Arg	Asp	Ile	Leu	Val	Glu				
Ala	Asp	Gly	Ala	Trp	Val	Val	Lys	Met	Phe	Tyr	Ser	Phe	Gln	Asp	Lys				
145	Arg	Asn	Leu	Tyr	Leu	Ile	Met	Glu	Phe	Leu	Pro	Gly	Gly	Asp	Met				
Thr	Leu	Leu	Met	Met	Lys	Lys	Asp	Thr	Leu	Thr	Glu	Glu	Glu	Thr	Gln				
Tyr	Ile	Ser	Glu	Thr	Val	Leu	Ala	Ile	Asp	Ala	Ile	His	Gln	Leu	Gly				
Phe	Ile	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Leu	Leu	Leu	Asp	Ala	Lys				
225	Gly	His	Val	Lys	Leu	Ser	Asp	Phe	Gly	Ser	Cys	Thr	Gly	Leu	Lys				
Ala	His	Arg	Thr	Glu	Phe	Tyr	Arg	Asn	Leu	Thr	His	Asn	Pro	Pro	Ser				
Asp	Phe	Ser	Phe	Gln	Asn	Met	Asn	Ser	Lys	Arg	Lys	Ala	Glu	Thr	Trp				
Lys	Lys	Asn	Arg	Arg	Gln	Leu	Ala	Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp				
Tyr	Ile	Ala	Pro	Glu	Val	Phe	Met	Gln	Thr	Gly	Tyr	Asn	Lys	Leu	Cys				
Asp	Trp	Trp	Ser	Leu	Gly	Val	Ile	Met	Tyr	Glu	Met	Leu	Ile	Gly	Tyr				
305	Pro	Pro	Phe	Cys	Ser	Glu	Thr	Pro	Gln	Glu	Thr	Tyr	Arg	Lys	Val				
Asn	Trp	Lys	Glu	Thr	Leu	Val	Phe	Pro	Glu	Pro	Glu	Val	Pro	Ile	Ser				
Lys	Ala	Lys	Asp	Leu	Ile	Leu	Arg	Phe	Cys	Ile	Asp	Ser	Glu	Asn	Arg				
Ile	Gly	Asn	Ser	Gly	Val	Glu	Ile	Lys	Gly	His	Pro	Phe	Phe	Glu	Ile				
385	Glu	Val	Asp	Trp	Glu	His	Ile	Arg	Glu	Arg	Pro	Ala	Ala	Ile	Pro				
Glu	Ile	Lys	Ser	Ile	Asp	Asp	Thr	Ser	Asn	Phe	Asp	Asp	Phe	Pro	Glu				
Ser	Ser	Ile	Leu	Gln	Pro	Val	Pro	Asn	Thr	Thr	Glu	Pro	Asp	Tyr	Lys				
Ser	Lys	Asp	Trp	Val	Phe	Leu	Asn	Tyr	Thr	Tyr	Lys	Arg	Phe	Glu	Gly				
Leu	Thr	Gln	Arg	Gly	Ser	Ile	Pro	Thr	Tyr	Met	Lys	Ala	Gly	Lys	Leu				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSN06  
(B) CLONE: 827431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Leu	Leu	Leu	Lys	Lys	His	Thr	Glu	Asp	Ile	Ser	Ser	Val	Tyr	Glu
1				5					10					15	
Ile	Arg	Glu	Arg	Leu	Gly	Ser	Gly	Ala	Phe	Ser	Glu	Val	Val	Leu	Ala
			20					25					30		
Gln	Glu	Arg	Gly	Ser	Ala	His	Leu	Val	Ala	Leu	Lys	Cys	Ile	Pro	Lys
		35					40					45			

Lys Ala Leu Arg Gly Lys Glu Ala Leu Val Glu Asn Glu Ile Ala Val  
 50 55 60  
 Leu Arg Arg Ile Ser His Pro Asn Ile Val Ala Leu Glu Asp Val His  
 65 70 75 80  
 Glu Ser Pro Ser His Leu Tyr Leu Ala Met Glu Leu Val Thr Gly Gly  
 85 90 95  
 Glu Leu Phe Asp Arg Ile Met Glu Arg Gly Ser Tyr Thr Glu Lys Asp  
 100 105 110  
 Ala Ser His Leu Val Gly Gln Val Leu Gly Ala Val Ser Tyr Leu His  
 115 120 125  
 Ser Leu Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Tyr  
 130 135 140  
 Ala Thr Pro Phe Glu Asp Ser Lys Ile Met Val Ser Asp Phe Gly Leu  
 145 150 155 160  
 Ser Lys Ile Gln Ala Gly Asn Met Leu Gly Thr Ala Cys Gly Thr Pro  
 165 170 175  
 Gly Tyr Val Ala Pro Glu Leu Leu Glu Gln Lys Pro Tyr Gly Lys Ala  
 180 185 190  
 Val Asp Val Trp Ala Leu Gly Val Ile Ser Tyr Ile Leu Leu Cys Gly  
 195 200 205  
 Tyr Pro Pro Phe Tyr Asp Glu Ser Asp Pro Glu Leu Phe Ser Gln Ile  
 210 215 220  
 Leu Arg Ala Ser Tyr Glu Phe Asp Xaa Pro Phe Trp Asp Asp Ile Ser  
 225 230 235 240  
 Glu Ser Gly Lys Asp Phe Ile Arg His Leu Leu Glu Arg Asp Leu Gln  
 245 250 255  
 Lys Arg Phe Thr Cys Gln Gln Ala Leu Arg Asp Leu Trp Ile Phe Trp  
 260 265 270  
 Asp Thr Gly Phe Gly Arg Asp Ile Leu Gly Phe Val Ser Glu Gln Ile  
 275 280 285  
 Arg Lys Asn Phe Ala Trp Thr His Trp Lys Arg Ala Phe Asn Ala Thr  
 290 295 300  
 Leu Phe Leu Arg His Ile Arg Lys Leu Gly Gln Ile Pro Glu Gly Glu  
 305 310 315 320  
 Gly Ala Ser Glu Gln Gly Met Xaa Arg His Ser His Xaa Gly Leu Arg  
 325 330 335  
 Ala Gly Gln Pro Pro Lys Trp  
 340

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNUT03  
 (B) CLONE: 1340712

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ile Leu Ala Ser Val Leu Arg Ser Gly Pro Gly Gly Leu Pro  
 1 5 10 15  
 Leu Arg Pro Leu Leu Gly Pro Ala Leu Ala Leu Arg Ala Arg Ser Thr  
 20 25 30  
 Ser Ala Thr Asp Thr His His Val Glu Met Ala Arg Glu Arg Ser Lys  
 35 40 45  
 Thr Val Thr Ser Phe Tyr Asn Gln Ser Ala Ile Asp Ala Ala Ala Glu  
 50 55 60  
 Lys Pro Ser Val Arg Leu Thr Pro Thr Met Met Leu Tyr Ala Gly Arg  
 65 70 75 80  
 Ser Gln Asp Gly Ser His Leu Leu Lys Ser Ala Arg Tyr Leu Gln Gln  
 85 90 95

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Glu Leu Pro Val Arg Ile Ala His Arg Ile Lys Gly Phe Arg Cys Leu
100 105 110

Pro Phe Ile Ile Gly Cys Asn Pro Thr Ile Leu His Val His Glu Leu
115 120 125
Tyr Ile Arg Ala Phe Gln Lys Leu Thr Asp Phe Pro Pro Ile Lys Asp
130 135 140
Gln Ala Asp Glu Ala Gln Tyr Cys Gln Leu Val Arg Gln Leu Leu Asp
145 150 155 160
Asp His Lys Asp Val Val Thr Leu Leu Ala Glu Gly Leu Arg Glu Ser
165 170 175
Arg Lys His Ile Glu Asp Glu Lys Leu Val Arg Tyr Phe Leu Asp Lys
180 185 190
Thr Leu Thr Ser Arg Leu Gly Ile Arg Met Leu Ala Thr His His Leu
195 200 205

Ala Leu His Glu Asp Lys Pro Asp Phe Val Gly Ile Ile Cys Thr Arg
210 215 220
Leu Ser Pro Lys Lys Ile Ile Glu Lys Trp Val Asp Phe Ala Arg Arg
225 230 235 240
Leu Cys Glu His Lys Tyr Gly Asn Ala Pro Arg Val Arg Ile Asn Gly
245 250 255
His Val Ala Ala Arg Phe Pro Phe Ile Pro Met Pro Leu Asp Tyr Ile
260 265 270
Leu Pro Glu Leu Leu Lys Asn Ala Met Arg Ala Thr Met Glu Ser His
275 280 285
Leu Asp Thr Pro Tyr Asn Val Pro Asp Val Val Ile Thr Ile Ala Asn
290 295 300
Asn Asp Val Asp Leu Ile Ile Arg Ile Ser Asp Arg Gly Gly Gly Ile
305 310 315 320
Ala His Lys Asp Leu Asp Arg Val Met Asp Tyr His Phe Thr Thr Ala
325 330 335
Glu Ala Ser Thr Gln Asp Pro Arg Ile Ser Pro Leu Phe Gly His Leu
340 345 350
Asp Met His Ser Gly Ala Gln Ser Gly Pro Met His Gly Phe Gly Phe
355 360 365

Gly Leu Pro Thr Ser Arg Ala Tyr Ala Glu Tyr Leu Gly Gly Ser Leu
370 375 380
Gln Leu Gln Ser Leu Gln Gly Ile Gly Thr Asp Val Tyr Leu Arg Leu
385 390 395 400
Arg His Ile Asp Gly Arg Glu Glu Ser Phe Arg Ile
405 410

```

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Leu Glu Lys Leu Glu Phe Glu Asp Glu Ala Val Glu Asp Ser Glu
1 5 10 15
Ser Gly Val Tyr Met Arg Phe Met Arg Ser His Lys Cys Tyr Asp Ile
20 25 30
Val Pro Thr Ser Ser Lys Leu Val Val Phe Asp Thr Thr Leu Gln Val
35 40 45
Lys Lys Ala Phe Phe Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro
50 55 60

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Leu Trp Glu Ser Lys Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr
65      70      75      80
Asp Phe Ile Asn Ile Leu His Arg Tyr Tyr Lys Ser Pro Met Val Gln
85      90      95
Ile Tyr Glu Leu Glu Glu His Lys Ile Glu Thr Trp Arg Glu Leu Tyr
100      105      110
Leu Gln Glu Thr Phe Lys Pro Leu Val Asn Ile Ser Pro Asp Ala Ser
115      120      125
Leu Phe Asp Ala Val Tyr Ser Leu Ile Lys Asn Lys Ile His Arg Leu
130      135      140
Pro Val Ile Asp Pro Ile Ser Gly Asn Ala Leu Tyr Ile Leu Thr His
145      150      155      160
Lys Arg Ile Leu Lys Phe Leu Gln Leu Phe Met Ser Asp Met Pro Lys
165      170      175
Pro Ala Phe Met Lys Gln Asn Leu Asp Glu Leu Gly Ile Gly Thr Tyr
180      185      190
His Asn Ile Ala Phe Ile His Pro Asp Thr Pro Ile Ile Lys Ala Leu
195      200      205

Asn Ile Phe Val Glu Arg Arg Ile Ser Ala Leu Pro Val Val Asp Glu
210      215      220
Ser Gly Lys Val Val Asp Ile Tyr Ser Lys Phe Asp Val Ile Asn Leu
225      230      235
Ala Ala Glu Lys Thr Tyr Asn Asn Leu Asp Ile Thr Val Thr Gln Ala
245      250      255
Leu Gln His Arg Ser Gln Tyr Phe Glu Gly Val Val Lys Cys Asn Lys
260      265      270
Leu Glu Ile Leu Glu Thr Ile Val Asp Arg Ile Val Arg Ala Glu Val
275      280      285
His Arg Leu Val Val Val Asn Glu Ala Asp Ser Ile Val Gly Ile Ile
290      295      300
Ser Leu Ser Asp Ile Leu Gln Ala Leu Ile Leu Thr Pro Ala Gly Ala
305      310      315      320
Lys Gln Lys Glu Thr Glu Thr Glu
325

```

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: HUVENOB01
- (B) CLONE: 39043

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

TACTCGGCAC CAGAGGCCAG GGTGCGAGGA CCACGGGCCGG CTCGGACGTG TGACCCGCGCC      60
TAGGGGGGTGG CAGCCGGGCGAG TCGCGGGGCGG CAAGGCGGACC ATGGAGCTTT TGGCGACTPAT      120
CACCTACCAGC CCAGCCGCCCA GCACCAAAAT GTGCGAGCAGC GCCTGGGGCA AGGGTTGCGG      180
AGCGGACTCG AAGAAGAAGC GGCCCGCCCA GCCCCCCGAC GAATCGCAGC CACCTCAGTC      240
CCAGGCGCAA GTGCCCCCGG CGGCCCTCA CACCATCAC CACCATTCGC ACTCGGGGCC      300
GGGATCTCG CGGATTATCG TCGACCCCCAC GACTGGGAAG CGTACTGCC GGGGCAAAAGT      360
GCTGGGAAGG GGTGGCTTTG CAAAATGTTA CGAGATGACA GATTTGACAA ATAACAAAGT      420
CTACGCCGCA AAAATTATTC CTCACAGCAG AGTAGCTAAA CCTCATCAA GGGAAAAGAT      480
TGACAAAGAA ATAGAGCTTC ACAGAATCTC TCATCATAAG CATGTAGTGC AGTTTATACA      540
CTACTTTCAG GACAAAGAAA ACATTATACAT TCTCTTGGAA TACTGCAGTA GAAGGTCAAT      600
GGCTCATATT TTGAAGACAA GAAAGGTGTT GACAGAGCCA GAAGTTCGAT ACTACCTCAG      660
GCAGATTGTG TCTGGACTGA AATACCTTCA TGAACAAGAA ATCTTGACA GAGATCTCAA      720
ACTAGGGAAC TTTTATTATA ATGAAGCCAT GGAACATAAA GTTGGGGACT TCGGCTTCGC      780
AGCCAGGCTA GAACCCCTGG AACACAGAAG GAGAACGATA TGTGGTACCC CAAATATCTC      840
CTCTCTGAA GTCTCAACA AACAGGACA TGGCTGTGAA TCAGACATTT GGGCCCTGGG      900
CTGTGTAATG TATACAATGT TACTAGGGAG GCCCCCATTT GAAACTACAA ATCTCAAGA      960

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AACCTTATAGG	TGCATAAGGG	AAGCAAGGTA	TACAATGCCG	TCCTCATTCG	TGGCTCCITGC	1020
CAGACACTTA	ATTTGCTAGTA	TGTTGTCCAA	AAACCCAGAG	GATCTGTCCA	GTTTGGATGA	1080
CATCATTCGA	CATGACCTTTT	TTTTGCGAGG	CTTCACTCCG	CACAGACTGT	CTTTCTAGCTG	1140
TTGTCTATACA	GTTCAGAGTT	TCCACTTATC	AAGCCCCAGT	AAGAATTCTC	TTAAGAAAGC	1200
AGCTGCTGCT	CTTTTGTGGT	GCAAAAAAGA	CAAAAGCAAGA	TATATTGACA	CACATAAATG	1260
AGTGTCTAAA	GAAAGATAGA	ACATCTACAA	GCTTAGGCAT	GATTTGAAAA	AGACTTCAAT	1320
AACTCAGCAGA	CCGAGCAAAAC	ACAGGACAGA	TGAGGAGCTC	CAGCCACCTA	CCACCACAGT	1380
TGCCAGGTCT	GGAAACCCCG	CAGTAGAAAA	CAAGCAGCAG	ATTGGGGATG	CTATTCCGAT	1440
GATAGTCAGA	GGGACTCTTG	GCAGCTGTAG	CAGCAGCAGT	GAATGCCTTG	AAGACAGTAC	1500
CATGGGAAGT	GTTCGCAGACA	CAGTGGCAAG	GGTTCCTCGG	GGATGTCTGG	AAAAACATGCC	1560
GGAGCTGTAT	TGCATTCCCA	AAGAGCAGCT	GAGCACATCA	TTTCAGTGGG	TCACCAAAATG	1620
CGTTTGATTAC	TCTAACAAAT	ATGGCTTTGG	GTACCAGCTC	TCAGACCACA	CCGTCGGGTG	1680
CGTTTTCACAT	AATGGTGCTC	ACATGAGCCT	CCTTCCAGAC	AAAAAAACAG	CTCATTATTA	1740
CCGACAGCTT	GGCCAAGTCT	CAGTTTTCCC	AGCAACAGAT	GCTCCTGAGC	AATTTATTAG	1800
TCAGATGTACG	GTGCTGAAAT	ACTTTTCTCA	TTACATGGAG	GAGAACCTCA	TGGATGGTGG	1860
AGATCTGCCT	AGTGTACTG	ATATTGGAAG	ACCTCGGCTC	TACCTCCTTC	AGTGGCTAAA	1920
ATCTGATACG	GCCTTAATGA	TGCTCTTTAA	TGATGGCACC	TTTCAGGTGA	ATTCTTACCA	1980
TGATCATAGA	AAAAATCAAG	TCTGTAGCCA	AAATGAAGAA	TACCTTTCTCA	CCTCAATCAA	2040
TGAGATATAGG	ATATTCTACAA	CTTTTCAGGCT	GACAACCTCT	CTGATGTCTG	GCTGTTCATC	2100
AGAAATAAAA	AATCGAATGG	AATATGCCCT	GAACATGCTC	TTTACAAAGAT	GTAACTGAAA	2160
GACTTTTCGA	ATFGACCTTA	TGGGACTCCT	CTTTTCCACT	GTGAGATTCA	CAGGGAAGCC	2220
AAAAAATGA	TCTAGAGCTA	GTGGAAGAG	ATGGACATGT	GGTGGTACGA	AACAAATTCC	2280
CTGTGGGCTC	GCTGAGTCTG	GTGGAACCCAG	AACAGGCTAA	GGCATACAGT	TCCTTGACITT	2340
GGACAATCCA	AGAGTAGAAC	AGAATGCAGT	TTTCCCTTGG	ATACCTGTGT	TAAAGGPTT	2400
TTTCAGACAA	TTTGCAGAAA	GCTGCATTGA	TTCTTAAAT	CTCTCTGTGT	AGAGCATTC	2460
AGCCAGAGGA	CTTTGGAAC	GTGAATATAC	TTCTCTGAAG	GGAGGGAGAA	GGGAGGAATC	2520
TCCCATGTGT	TTTAAAGGCT	GTAATTGGAG	CAGCTTTTGG	CTCGGTATG	GTGAACATATG	2580
GCCATATATA	ATTTTPTTCT	ATTAATTTT	GAAAGTACTT	GTGGCTGGATA	AGAGTCATTC	2640
CTTTGTAATA	AACCTTTTAT	TTATTACAGC	CCAAAGAGCA	GTATTTTTAA	TCAAAATGTC	2700
TTTTTTTATA	TGTTGACCAT	TTTAAACCGT	TGGCAATAAA	GAGTATGAAA	ACGCAGAAAA	2760
AAAAAAAAAA						2770

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1593 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vi) IMMEDIATE SOURCE:

- (A) LIBRARY: TBLYN0701  
 (B) CLONE: 40194

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAGGCGTCC	CTTCTACTC	ACGTTTGCCA	AAAGCGGGTC	CGAGCTGTGA	CGGGAAAAAA	60
GTGATGCCAC	CAAAAAGTAA	TGAAAAATAC	AAACTTCCCT	TTCCATTTC	AGAAGGCAAG	120
GTCTCTGGATG	ATATGGAAGG	CAATCAGTGG	GTACTGGGCA	AGAAGATTGG	CTCTGGAGAG	180
TTTGGAATGA	TATATTAGC	TTTCCCACA	AATAAACCCAG	AGAAAGATGC	AAGACATGTA	240
GTAAAAGTGG	AATATCAGA	AAATGGCCCG	TTATTTCGAC	TATAGAACGA	AACAACTTGA	300
GTGTCAAAAA	AAGACTGTAT	CAAAAAGTGG	TATAGAACGA	AACAACTTGA	TTATTTTAGGA	360
ATTTCCTCTGT	TTATGTGAAT	TGGTCTGACT	GAATTCGAAG	GAAGAAGTTA	CAGATTATGT	420
GTAAATGGAAA	GACTAGAAAT	AGATTACAG	AAGATTCTAG	GCCCAATATG	TAGCAATTAAA	480
AAGTCAACTG	TCTTCAATT	AGGATCCGA	ATGTTGGATG	TACTGGAAAT	TATACATGTA	540
AATGAATATG	TTCAATGTGA	TGTAAGAACGA	ACAACTCTAC	TTTGGGATTA	TACCAATATCA	600
GACCAAGTTT	ATCTTGCAGA	TTATGGACTT	TCCATACAGT	ATTGTCCCAA	TGGGAACACC	660
AAACAGTATC	AGGAAAATCC	TAGAAAAGGC	CATAATGGGA	CAATAGAGTT	TACCAAGCTTG	720
GATGCCCCACA	AGGGAGTAGG	TGAAATAGCC	CAATTTTGG	TATGTGCTCA	TAGTTTAGCA	780
TATGATGAAA	AGCCAACTA	TCAAGCCCTC	AAGAAAATTT	TGAACCTTCA	TGGAATTACCT	840
TTAGGACAC	TGACTTTTTC	CACAAAAGGA	CAGAGTATAA	ATGTCCATAC	TCCAAACAGT	900
CAAAAAGTTG	ATTCAACAAA	GGCTGCAACA	ACAAAGTCA	ACAAAGGACA	CAATAGATGA	960
ATCGAAAAAA	AAGTCCACAG	TGAGAGGAAG	GCTGAGTCCT	GTGCAACATG	GAAAGTGCAG	1020
AAAGAGGAGA	AACATGATGG	ATTGATGAAC	AATGAAGCAG	CTCAGGAAAG	CACAAGGAGA	1080
AGACAGAAAT	ATCAAGAGTC	TCAAGAACCT	TGGAATGAAG	TAAACAGTTT	CCCACAAAAA	1140
ATCAGCTATA	CACAATTCCC	AAACTCATTT	TATGAGCCTC	ATCAAGATTT	TACCAGTCCA	1200

GATATATTCA	AGAAGTCAAG	ATCTCCATCT	TGGTATAAAT	ACACTTCCAC	AGTCAGCAGC	1260
GGGATACAG	ACTTAGAAAG	TTCAACTGGA	CTTTGGCCTA	CAATTTCCCA	GTTTACTCTT	1320
AGTGAAGAGA	CAAAACGAGA	TGTTTATTAT	TATCGCATCA	TCATACCTGT	CCTTTTGATG	1380
TTAGTATTTC	TTGCTTTTAT	TTTCTCTCTA	AGATGATACC	AAAATTCCTT	TTGATAATTT	1440
TTTAAGTTTC	CAGCTCTTCA	CCGAAATGTT	GTATTCTTAT	TTCAAGTGTTT	CCTTCCAGAC	1500
ATTTTAAAG	TAAATGGCTT	TAAAAAGAGA	ACATATTTTA	ACAAAGTTTG	TGGACACTCT	1560
AAAAAATAAA	ATTGCTTTGT	ACTAGAAAAA	AAA			1593

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: TMLR3DT01  
 (B) CLONE: 402339

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGCCCCGG	GAGCCCCGAT	GCTGGCCCCG	AGGAAGCCGG	TGCTGCCCGC	GCTCACCATC	60
AACCTTACCA	TCGCCGAGGG	CCCATCCCTT	ACCAGCGAGG	GCCTCTCCGA	GGCAAACTGT	120
GTGGACCTGC	AGAAGAAGCT	GGAGGAGCTG	GAACCTTGAG	AGCAGCAGAA	GAAGCGGCTG	180
GAAGCCTTTC	TCACCCAGAA	AGCCAAGGTC	GGCGAACTCA	AAGACGATGA	CTTTCGAAAGG	240
ATCTCAGAGC	TGGCGCGGGG	CAACGGCCGG	GTGGTCAACA	AAGTCCAGCA	CAGACCCCTCG	300
GGCCTCATCA	TGGCCAGGAA	GCTGATCCAC	CTTGAGATCA	AGCCGGCCAT	CCGGAACAG	360
ATCATCCCGG	AGCTGCAGGT	CCTGCACGAA	TGCAACTCGC	CGTACATCGT	GGCTTCTPAC	420
GGGGCCTTCT	ACAGTGAAGG	GGAGATCAGC	ATTTGCATGG	AACACATGGA	CGCGGGCTCC	480
CTGGACCATC	CGCTGAAAGA	GGCCAAGAGG	ATTCCCGAGG	AGATCTCTGG	GAAAGTCAGC	540
ATCGCGTTTC	TCCGGGGCTT	GGCGTACCTC	CGAGAGAAGC	ACCAGATCAT	GACCCGAGAT	600
GTGAAGCCCT	CCAACATCTT	CGTGAACCTT	AGAGGGGAGA	TCAAGCTGTG	TGACTTTCGGG	660
GTGAGCGGCC	AGCTCATCGA	CTCCATGGCC	AACCTCTCTG	TGGGCGCGGG	CTCTCTACATG	720
GCTCCGGAGC	GGTTGCAGGG	CACACATTAC	TCGGTGCAGT	CGGACATCTG	GAGCATGGGC	780
CTGTCCCTTG	TGGAGCTGGC	CGTCGGAAGG	TACCCCATCC	CCCCGCCCCG	CGCCAAAGAG	840
CTGGAGGCCA	CTTTTGGCCG	GCCTCTGGTC	GACGGGGAAG	AAGGAGAGCC	TCACAGCATC	900
TCGCCCTCGC	CGAGGCCCCC	CGGGCGCCCC	GTCAGCGGTC	ACGGGATGGA	TAGCCGGGCT	960
GCCATGGCCA	TCCTTGAAC	CCTGGACTAT	ATTGTGAAGC	AGCCACCTCC	TAAGCTGCCCT	1020
AACGGTGTGT	TCACCCCGGA	CTTCCAGGAG	TTTGTCAATA	AATGCCATAT	CAAGAACCCA	1080
GCGGAGCGGG	CGGACCTGAA	GATGCTCACA	AACCACACCT	TCATCAAGCG	GTCCTGAGGTG	1140
GAGAAGTGG	ATTTTGGCGG	CTGGTGTGT	AAAACCTCGC	GGCTGAACCA	GCCCGGCACA	1200
CCCAACGCCA	CCGCGGTGTG	ACAGTGGCCG	GGCTCCCTGC	GTCCTCGCTG	TGACCTGCCC	1260
ACCGTCCCTG	TCCATGCCCC	GCCTTCCAG	CTGAGGACAG	GCTGGCGCCT	CCACCCACCC	1320
TCCTCCCTCA	CCCTTCCGGA	GAGCACCGTG	CGCGGGCGCA	AGCGCATGCA	GGAACGGGGG	1380
TCCTCTCTCC	TGCCGCTCCT	GGCCGGGGTG	CCTCTGGGGA	CGGGCGACGC	TGCTGTGTGT	1440
GGTCTCAGAG	GCTCTGCTTC	CTTAGGTTAC	AAAACAAAC	AGGGAGAGAA	AAAGCAAAAA	1500
AAAA						1504

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1935 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SYNORAT04  
 (B) CLONE: 705365

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGAGGCTG	AGCCGCGCCG	GGCGCGGACC	GGAGGCACTT	TCCGTTACTA	TGGCAATGAC	60
GGCAGGGACT	ACAACAACCT	TTCTTATGAG	CAACCATACC	CGGGAAAGAG	TGACTGTAGC	120
CAGCTCTACA	TGGGAATTT	TTTATAGCAA	CCTAATTTTA	CAGCATGAAG	AGAGAGAAAC	180

CAGGCAGAAG	AAATAGAAAG	TGGCCATGGA	AGAAGAAGGA	TTAGCAGATG	AAGAGAAAAA	240
GTTACGTCGA	TCACAACACG	CTCGCAAAAG	AACAGAGTTC	TTACGGCTCA	AAAGGACCAG	300
ACTTGGCTTG	GATGACTTTG	AGTCTCTGAA	AGTTATAGGA	AGAGGAGCTT	TTGGGAGAGT	360
CGGGTGGCTG	CACAAAAAAG	ATACAGGCCA	TATCTATGCA	ATGAAGATAT	TGAGAAAGGT	420
TGATATGCTT	GAAGAAAGAG	AGGTGGCCCA	TATCCGAGCA	GAAGAGATA	TTTTGGTAGC	480
AGCAGATGGT	GCCTGGGTGG	TGAAGATGTT	TTACAGTTTT	CAGGATAAGA	GGAACTTTTA	540
TCTAATCATG	GAATTTCTCC	CTGGAGGTGA	CATGATGACA	TTGCTAAATG	AGAAAGACAC	600
CTTGACAGAA	GAGGAAACAC	AGTTCTACAT	TTCAGAGACT	GTTCGGCAA	TAGATCCGAT	660
CCACCAGTTG	GGTTTCTATC	ATCGGGATAT	TAAGCCAGAC	AACTTTTAT	TGGATGCCAA	720
GGGTCTATGA	AAATTTATCT	ATTTTGGTTC	ATGTACGGGA	TTAAAGAAAG	CTCAGGACAG	780
TGAATTTTAT	AGAAATCTCA	CACACAACCC	ACCAAGTGAC	TTCTCATTTT	AGAACATGAA	840
CTCAAGAGAG	AAAGCAGAAA	CTTGGGAAGAA	GAACAGGAGA	CAACTGGCAT	ATTCACAGCT	900
TGGGACAGCA	GATTACATCT	CTCCAGAAAT	ATTCTATGCA	ACTGGTTTAC	ACAAATTTGT	960
TGACTGGTGG	TCTTTGGGAG	TGATTTATGA	TGAAATGCTA	ATAGGATATC	CACCTTTTCT	1020
CTCTGAAACA	CCTCAAGAAA	CATACAGAAA	AGTGATGAAC	TGGAAAGAAA	CTCTGGTATT	1080
TCCTCAGAGC	GTACTATAT	CTGAGAAAGC	CAAGGACTTA	ATTCTCAGAT	TTTTGATTGA	1140
TTCTGAAACG	AGAAATGGAA	ATAGTGGAGT	AGAGAAATA	AAAGGTCATC	CCTTTTGTGA	1200
AGGTGTGCGC	TGGGAGCAGA	TGAAGGAAAG	GCCAGCAGCA	ATCCCATATG	AAATCAAAAG	1260
CATTGATGAT	ACTTCAAATT	TTGATGACTT	CCCTGAATCT	GATATTTTAC	AACCAAGTCC	1320
AAATACCCAG	GAACCGGACT	ACAAATCCAA	AGACTGGGTT	TTTCTCAATT	ATACCTATAA	1380
AAGGTTTGAA	GGGTTGACTC	AACGTGGCTC	TATCCCACCC	TACATGAAAG	CTGGGAAGTT	1440
ATGAATGAAG	ATPACMTTCA	CCCATAACCA	AGAGAAGCTA	GGTAGCTGCA	TCCACAGGCT	1500
TGCTTGGCGT	AGATAACAA	ACACTGAAAT	ACTCCTGAAG	ATGGTGGTGC	TTATTGACTA	1560
CAAGAGGAGA	TCTACAGAG	TTAGGATTTC	TAAGACTACT	ATAGGAATTG	CTCCAGCATG	1620
CCAGCTGGCT	CTTTTCTTTA	ATATTTTAT	ATTTTGTGTA	ACTTTTATAT	ATGAAGGTAT	1680
TGGAATAAAA	GGAGCAAGCA	TCCCTTTCTA	ACTGCACCTG	CTACATCGGT	TTTTAGGTTCC	1740
ATTCGCTCTG	TGTGTGCTGT	GGCTTTGAAC	TGTAACACCT	CTAATCAATT	CAGGAGAAAC	1800
ACATATCAT	TAAAGCAACA	TAGGCTAACC	TGTANGTAAC	ACTCGAGTAT	TGATGTTTFA	1860
CTGCAAAATC	TATGGGTCTA	GATAATCAGT	AAAAGCCATC	TTCCATAGTT	GGTGTTAGAA	1920
CATTGCCCTA	TTGGT					1935

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSN0T06
- (B) CLONE: 827431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAATTTCCT	ACTAGGGTCT	TCTCTGGCCC	AGCCTTTGAC	TGAAGCTGGT	CTGGAGACAG	60
GGCAATTTCG	GAAGTGAATC	ATAGATGGCC	TAAAGAAAGC	GGGCCATCTA	AGGACCCAGG	120
ACAGAGGGAA	GAGGGCCAA	CCAGCTGGAC	CACAGGCAAA	CCCATTTGCC	TTTGAGAGAA	180
AGAAGAGGAC	CCGGTGAAC	ATGCTGCTGC	TGAAGAAACA	CACGGAGGAC	ATCAGCAGG	240
TCTACGAGAT	CCCGGAGAGG	CTCGGCTCGG	GTGCCCTTCT	CGAGGTGGTG	CTGGCCGAGG	300
AGGCGGCCTC	CGCACACCTC	GTGGCCCTCA	AGTGCACTCC	CAAGAAGGCC	CTCCGGGGCA	360
AGGAGGCCCT	GGTGGAGAAC	GAGATCGCAG	TGCTCCGTAG	GATCAGTAC	CCCAACATCG	420
TGCTCTGCGA	GGATGTCCAC	GAGAGCCCTT	CCCACTCTA	CCTGGCCATG	GAATCTGTGA	480
CGGGTGGCGA	CGTGTGTTGAC	CGCATCATGG	AGCCCGGCTC	CTACACAGAG	AAGGATGCCA	540
GCATCTGTGT	GGGTCAAGTTC	CTTGGCGCCG	TCTCTACCT	GCACAGCCCTG	GGGATCTGTC	600
ACCGGAGGCT	CAAGCCCGAA	AACTTCTGTT	ATGCCACGCC	CTTTGAGGAC	TCCAGATCTA	660
TGGTCTCTGA	CTTTGGAGTC	TCCAAAATCC	AGGCTGGGAA	CAATGTAAGC	ACCCCTGTG	720
GGAGCCCTGG	ATATGTGGCC	CCAGAGCTCT	TGGAGCAGAA	ACCTTACGGG	AAGCCGCTAG	780
ATGTGTGGGC	CTTGGGCGTC	ATCTCTTACA	TCTTGTGTGT	TGGGTACCCC	CCCTTTCTAG	840
ACGAGAGCGA	CCCTGAGCTC	TTGAGCCAGA	TCTGAGGGC	CAGCTATGAG	TTTGACTNTC	900
CTTTCTGGGA	TGACATCTCA	GAATCAGGCA	AAGACTTTAT	CTGGCACCCT	CTGGAGCGAG	960
ACCTTTCAGAA	GAGGTTTACC	TGCCAACAGG	CCTTGGCGGA	CTTTTGGATC	TTTTGGGACA	1020
CAGGCTTTGG	CAGGGACATC	TTAGGGTTTG	TGAGTGAAGA	GATCCGGGAA	AACTTTGCTT	1080
GGACACACTG	GAGGCGAGCC	TTCAATGCCA	CCTTTGCTCT	GGCCACATCA	CCGAAAGCTG	1140
GGCAGATCCC	AGAGGCGGAG	GGGGCTCTGT	AGCAGGGGAT	GGSCCGNAC	AGGCCATNAG	1200
GCCTTCTGTG	TGCGGACGCC	CCCAAGTGGT	GATGCCCAGG	NAGATGCCGA	GGCCAAGTGG	1260

ANTGANCCCC AGATTTNCTT NC

1282

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: COLNTUT03
- (B) CLONE: 1340712

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

CGCGCGAGGG CGCAGGCGGG TGGGCGCCTG CGGAGTGGAC TGTTCGAGCC CTTCGCTGG 60
GACCCGGGCC CTGGCTCCGG CCCCGCGATG GGAGCTGCTC TCCCGGGGCT GAGCGTGTCA 120
GCATCCTCGA CGCACCCTGG TCCCTGAAGT CGGAGAAGAG CCCCTACCCA CCCACACCCC 180
CTTGGCCCTT TTTGGGTCGC CTGGGTCTCT AGTCTAGCG GATCCTCAGT CCTAGCGGCC 240
ACCGGGCTTC AAAGAGACAA GACGATGATC CTGGCGTCCG TGCTGAGGAG CGGTCCCGGG 300
GGCGGGCTTC CGCTCCGGCC CCTCTGGGA CCGGCACTCG CGCTCCGGGG CCCTCGACG 360
TGGGCCACCG ACACACACCA CGTGGAGATG GCTCGGGAGC GCTCAACAGC CGTCACTTCC 420
TTTTACAAAC AGTCGSCCTG GACGCGCGCA GCGGAGAAGC CCTCAGTCCG CTTAACGGCCC 480
ACCATGATGC TCTACGCTGG CCGCTCTCAG GACGCGACCC ACCTTCTGAA AAGTGCTCGG 540
TACCTGCAGC AAGAAGCTTC AGTGAGGATT GCTCACCGCA TCAAGGGCTT CCCTGCTCTT 600
CCTTTCATCA TTGGCTGACG CCCACACATA CTGCACGTGC ATGAGCTATA TATCGCTGCC 660
TTCCAGAAGC TGACAGACTT CCCTCCGATC AAGGACCCAG CGGACGAGGC CCAGTACTGC 720
CAGCTGGTGC GACAGCTGCT GSGATGACCAC AAGGATGTGG TGACCTCTTT GGCAGAGGGC 780
CTACGTGAGA GCGCGAAGCA CATAGAGGAT GAAAAGCTCG TCCGCTACTT CTTCGACAA 840
ACGCTGACTT CGAGGCTTGG AATCCGCATG TTGGCCACGC ATCACTGGC GCTGCATGAG 900
GACAAGCCTG ACTTTGTCGG CATCATCTGT ACTCTCTCT CACCAAGAA GATTATTGAG 960
AAGTGGGTGG ACTTTGCCAG ACGCCTGTGT GAGCACAAGT ATGGCAATGC CCGCCGTGTC 1020
CGCATCAATG GCCATGTGGC TGCCCGGTTC CCCTTCATCC CTATGCCACT GGAATCATATC 1080
TGGCCGAGGC TGCTCAAGAA TGCCATGAGA GCCACAATGG AGAGCCACCT AGACACTCCC 1140
TACAATGTCC CAGATGTGGT CATCACCATC GCCACAATG ATGTCGATCT GATCATCAGG 1200
ATCTCAGACC GTGGTGGAGG AATCGCTCAC AAAGATCTGG ACCGGGATCT GGAATPACAC 1260
TTCACTACTG CTGAGGGCAG CACACAGGAC CCCCGGATCA GCCCCCTCTT TGCCCATCTG 1320
GACATGCATA GTGGCGCCCA CTCAGGACCC ATGCACGGGT TTGGCTTCGG GTTGCCACAG 1380
TCACGGGCTC ACGCGGAGTA CCTCGGTGGG TCTCTGCAGC TGCAGTCCCT GCAGGGCATT 1440
GGCAGCGACG TCTACCTGCG GCTCCGCCAC ATCGATGGCC GGGAGGAAAG CTTCCGATC 1500
TGACCCACCA GCCTTTGGCC TGCTCACCCG ACCAGCCTGG GCCGCATTC CTGACGAGCC 1560
TCCCGGGTCA GGCAGGGCGG CCCCCTGCTC CACACACTGC TGCATCTTGG GTCTCAGGGA 1620
CCGACGAGCA TGGACTTACA TGGAGCTGGG CACTGCCCTT GCCTCAACAG GGTTCATTGC 1680
TCTCTCGCCT CAGAACTTGG AGCAGGGAAG TGGGCACCTG AGGCCTCAGC ACAGTCTGCT 1740
CATTTCTCTT TGGGGGACCC CACTCTGAGC TGTATTATTA GTTCACATTT TGAATGGCC 1800
AGAAAAGAAG GAAGTGGATG GTTGTGTGAG AGGGTGTTGG AGAGGTGAGG TGTGTGTGTT 1866
TTGTGTGT

```

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENITUT01
- (B) CLONE: 1452972

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GGCCCCAGCG CTCGGCGCGG CGCAGGCCCC CGGCGCGGGG ACGAGCGTCG CAGCTCATGC 60
TGATCGCTGT CCTCTCTCTC CCCCTCAGGC GGGCGTGGCG GCGGCCCTGG GACCCGCGGA 120
AGCCGCGCAT CTGGAGAAGC TGGAGTTCGA GACGAGAACA GTAGAAGACT CAGAAAGTGG 180

```

TGTTTACATG	CGATTTCATGA	GGTCACACAA	GTGTTATGAC	ATCGTTCCAA	CCAGTTCCAA	240
GCTTTGTGTC	TTTGATACITA	CATTACAAGT	TAAAAAGGCC	TTCTTTTGCTT	TGGTAGCCAA	300
CGGTGTCGGA	GCAAGCGCAC	TGTGGGAGAG	TAAAAAACAA	AGTTTGTGTAG	GAATGCTAAC	360
AATTACAGAT	TTCATAAATA	TACTACATAG	ATACTATAAA	TCACCTATGG	TACAGATTTA	420
TGAATTAGAG	GAACATAAAA	TTGAAACATG	GAGSGAGCCT	TATTTACAAG	AAACATTAA	480
GCCTTTAGTG	AATATATCTC	CAGATGCAAG	CCTCTTCGAT	GCTGTATACT	CCTTCATTCA	540
AAATAAAATC	CACAGATTGC	CCGTTATTGA	CCCTATCAGT	GGGAATGCA	TTTATATACT	600
TACCCACAAA	AGAATTCCTCA	AGTTTCTCCA	GCTTTTATG	TCTGATATCT	CAAAGCCTGC	660
CTTTCATGAAG	CAGAACCTGG	ATGAGCTTGG	AATAGGAACG	TACCACAACA	TTGCCTTCAT	720
ACATCCAGAG	ACTCCCATCA	TCAAAGCCTT	GAACATATTT	TGTGAAAGAC	GAATATCAGC	780
TCTGCGCTGT	GTGGATGAGT	CAGGAAAAGT	TGTAGATATT	TATTCCAAAT	TTGATGTAAT	840
TAATCTTGCT	GCTGAGAAAA	CATACAATAA	CCTAGATATC	ACGGTGACCC	AGGCCCTTCA	900
GCACCGTTCA	CAGTATTTTG	AAGGTGTTGT	GAACTGCAAT	AAGCTGGAAA	TACTGGAGAG	960
CATCTGTGAC	AGAATAGTAA	GAGCTGAGGT	CCATCGGCTG	TGTGTGGTAA	ATGAAGCAGA	1020
TAGTATTGTC	GGTATTTAT	CCCTGTGCGA	CATTCTGC	GCCTGTATCC	TCACACCAGC	1080
AGGTGACAAA	CAAAAGGAGA	CAGAAACGGA	GTGACCGCGG	TGAATGTAGA	CGCCCTAGGA	1140
GGAGAACTTG	AACAAAGTCT	CTGGGTACAG	TTTTCGCTCA	TGAACACTGG	CTGCAAGTGG	1200
TTAAGAAATGT	ATATCAGGGT	TTAACAATAG	GTATTTCTTC	CAGTGATGTT	GAATTAAGC	1260
TTAAAAAAGA	AAGATTTTAT	GTGCTTGAAG	ATTCAGGCTT	GCATTTAAAG	ACTGTTTTCA	1320
GACCTTTGTC	TGAAGGATTT	TAAATGCTGT	ATGTCATTA	AGTGCACTGT	GCTCTGAAGT	1380
TTTCATTATT	TTTCATTTCA	AAGAAATCAC	TGGTATGGAA	CAGGTGATGT	GGCAT	1435

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1488263

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Leu	Ala	Gly	Leu	Pro	Thr	Ser	Asp	Pro	Gly	Arg	Leu	Ile	Thr	Asp
1				5					10					15	
Pro	Arg	Ser	Gly	Arg	Thr	Tyr	Leu	Lys	Gly	Arg	Leu	Leu	Gly	Lys	Gly
			20					25					30		
Gly	Phe	Ala	Arg	Cys	Tyr	Glu	Ala	Thr	Asp	Thr	Glu	Thr	Gly	Ser	Ala
			35				40					45			
Tyr	Ala	Val	Lys	Val	Ile	Pro	Gln	Ser	Arg	Val	Ala	Lys	Pro	His	Gln
			50			55					60				
Arg	Glu	Lys	Ile	Leu	Asn	Glu	Ile	Glu	Leu	His	Arg	Asp	Leu	Gln	His
65				70					75					80	
Arg	His	Ile	Val	Arg	Phe	Ser	His	His	Phe	Glu	Asp	Ala	Asp	Asn	Ile
			85						90					95	
Tyr	Ile	Phe	Leu	Glu	Leu	Cys	Ser	Arg	Lys	Ser	Leu	Ala	His	Ile	Trp
			100					105					110		
Lys	Ala	Arg	His	Thr	Leu	Leu	Glu	Pro	Glu	Val	Arg	Tyr	Tyr	Leu	Arg
			115				120						125		
Gln	Ile	Leu	Ser	Gly	Leu	Lys	Tyr	Leu	His	Gln	Arg	Gly	Ile	Leu	His
			130				135					140			
Arg	Asp	Leu	Lys	Leu	Gly	Asn	Phe	Phe	Ile	Thr	Glu	Asn	Met	Glu	Leu
145				150					155					160	
Lys	Val	Gly	Asp	Phe	Gly	Leu	Ala	Ala	Arg	Leu	Glu	Pro	Pro	Glu	Gln
			165						170					175	
Arg	Lys	Lys	Thr	Ile	Cys	Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val
			180					185						190	
Leu	Leu	Arg	Gln	Gly	His	Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Leu	Gly
			195				200					205			
Cys	Val	Met	Tyr	Thr	Leu	Leu	Cys	Gly	Ser	Pro	Pro	Phe	Glu	Thr	Ala
			210				215				220				
Asp	Leu	Lys	Glu	Thr	Tyr	Arg	Cys	Ile	Lys	Gln	Val	His	Tyr	Thr	Leu
225				230					235						

```

Pro Ala Ser Leu Ser Leu Pro Ala Arg Gln Leu Leu Ala Ala Ile Leu
      245      250      255
Arg Ala Ser Pro Arg Asp Arg Pro Ser Ile Asp Gln Ile Leu Arg His
      260      265      270
Asp Phe Phe Thr Lys Gly Tyr Thr Pro Asp Arg Leu Pro Ile Ser Ser
      275      280      285
Cys Val Thr Val Pro Asp Leu Thr Pro Pro Asn Pro Ala Arg Ser Leu
      290      295      300
Phe Ala Lys Val Thr Lys Ser Leu Phe Gly Arg Lys Lys Lys Ser Lys
      305      310      315      320
Asn His Ala Gln Glu Arg Asp Glu Val Ser Gly Leu Val Ser Gly Leu
      325      330      335
Met Arg Thr Ser Val Gly His Gln Asp Ala Arg Pro Glu Ala Pro Ala
      340      345      350
Ala Ser Gly Pro Ala Pro Val Ser Leu Val Glu Thr Ala Pro Glu Asp
      355      360      365
Ser Ser Pro Arg Gly Thr Leu Ala Ser Ser Gly Asp Gly Phe Glu Glu
      370      375      380
Gly Leu Thr Val Ala Thr Val Val Glu Ser Ala Leu Cys Ala Leu Arg
      385      390      395      400
Asn Cys Ile Ala Phe Met Pro Pro Ala Glu Gln Asn Pro Ala Pro Leu
      405      410      415
Ala Gln Pro Glu Pro Leu Val Trp Val Ser Lys Trp Val Asp Tyr Ser
      420      425      430
Asn Lys Phe Gly Phe Gly Tyr Gln Leu Ser Ser Arg Arg Val Ala Val
      435      440      445
Leu Phe Asn Asp Gly Thr His Met Ala Leu Ser Ala Asn Arg Lys Thr
      450      455      460
Val His Tyr Asn Pro Thr Ser Thr Lys His Phe Ser Phe Ser Val Gly
      465      470      475      480
Ala Val Pro Arg Ala Leu Gln Pro Gln Leu Gly Ile Leu Arg Tyr Phe
      485      490      495
Ala Ser Tyr Met Glu Gln His Leu Met Lys Gly Gly Asp Leu Pro Ser
      500      505      510
Val Glu Glu Val Glu Val Pro Ala Pro Pro Leu Leu Leu Trp Val
      515      520      525

Lys Thr Asp Gln Ala Leu Leu Met Leu Phe Ser Asp Gly Thr Val Gln
      530      535      540
Val Asn Phe Tyr Gly Asp His Thr Lys Leu Ile Leu Ser Gly Trp Glu
      545      550      555      560
Pro Leu Leu Val Thr Phe Val Ala Arg Asn Arg Ser Ala Cys Thr Tyr
      565      570      575
Leu Ala Ser His Leu Arg Gln Leu Gly Cys Ser Pro Asp Leu Arg Gln
      580      585      590
Arg Leu Arg Tyr Ala Leu Arg Leu Leu Arg Asp Arg Ser Pro Ala
      595      600      605

```

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 396 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 1827450

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met Pro Arg Val Lys Ala Ala Gln Ala Gly Arg Gln Ser Ser Ala Lys
1          5          10          15
Arg His Leu Ala Glu Gln Phe Ala Val Gly Glu Ile Ile Thr Asp Met
20          25          30

```

Ala Lys Lys Glu Trp Lys Val Gly Leu Pro Ile Gly Gln Gly Gly Phe  
 35 40 45  
 Gly Cys Ile Tyr Leu Ala Asp Met Asn Ser Ser Glu Ser Val Gly Ser  
 50 55 60  
 Asp Ala Pro Cys Val Val Lys Val Glu Pro Ser Asp Asn Gly Pro Leu  
 65 70 75 80  
 Phe Thr Glu Leu Lys Phe Tyr Gln Arg Ala Lys Pro Glu Gln Ile  
 85 90 95  
 Gln Lys Trp Ile Arg Thr Arg Lys Leu Lys Tyr Leu Gly Val Pro Lys  
 100 105 110

Tyr Trp Gly Ser Gly Leu His Asp Lys Asn Gly Lys Ser Tyr Arg Phe  
 115 120 125  
 Met Ile Met Asp Arg Phe Gly Ser Asp Leu Gln Lys Ile Tyr Glu Ala  
 130 135 140  
 Asn Ala Lys Arg Phe Ser Arg Lys Thr Val Leu Gln Leu Ser Leu Arg  
 145 150 155 160  
 Ile Leu Asp Ile Leu Glu Tyr Ile His Glu His Glu Tyr Val His Gly  
 165 170 175  
 Asp Ile Lys Ala Ser Asn Leu Leu Leu Asn Tyr Lys Asn Pro Asp Gln  
 180 185 190  
 Val Tyr Leu Val Asp Tyr Gly Leu Ala Tyr Arg Tyr Cys Pro Glu Gly  
 195 200 205  
 Val His Lys Glu Tyr Lys Glu Asp Pro Lys Arg Cys His Asp Gly Thr  
 210 215 220  
 Ile Glu Phe Thr Ser Ile Asp Ala His Asn Gly Val Ala Pro Ser Arg  
 225 230 235 240  
 Arg Gly Asp Leu Glu Ile Leu Gly Tyr Cys Met Ile Gln Trp Leu Thr  
 245 250 255  
 Gly His Leu Pro Trp Glu Asp Asn Leu Lys Asp Pro Lys Tyr Val Arg  
 260 265 270  
 Asp Ser Lys Ile Arg Tyr Arg Glu Asn Ile Ala Ser Leu Met Asp Lys  
 275 280 285  
 Cys Phe Pro Glu Lys Asn Lys Pro Gly Glu Ile Ala Lys Tyr Met Glu  
 290 295 300  
 Thr Val Lys Leu Leu Asp Tyr Thr Glu Lys Pro Leu Tyr Glu Asn Leu  
 305 310 315 320  
 Arg Asp Ile Leu Leu Gln Gly Leu Lys Ala Ile Gly Ser Lys Asp Asp  
 325 330 335  
 Gly Lys Leu Asp Leu Ser Val Val Glu Asn Gly Gly Leu Lys Ala Lys  
 340 345 350  
 Thr Ile Thr Lys Lys Arg Lys Lys Glu Ile Glu Glu Ser Lys Glu Pro  
 355 360 365  
 Gly Val Glu Asp Thr Glu Trp Ser Asn Thr Gln Thr Glu Glu Ala Ile  
 370 375 380  
 Gln Thr Arg Ser Arg Thr Arg Lys Arg Val Gln Lys  
 385 390 395

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 303804

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn Pro  
 1 5 10 15  
 Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu Ala



His Gln Gly Gly Ile	Leu Gln Glu Asn Met	Val Arg Glu Gly Ala	20	Asp	Leu	Gln	Lys	Lys	25	Leu	Glu	Glu	Leu	Asp	30	Leu	Asp	Glu																
			35							40					45																			
			50	Arg	Lys	Arg	Leu	Glu	Ala	Phe	Leu	Thr	Gln	Lys	Ala	Lys	Val																	
			65				Asp	Asp	Phe	Glu	Arg	Ile	Ser	Glu	Leu	Gly	Ala																	
			80			Val	Val	Thr	Lys	Ala	Arg	His	Arg	Pro	Ser	Gly	Leu																	
Ile	Met	Ala	Arg	Lys	Leu	Ile	His	Leu	Glu	Ile	Lys	Pro	Ala	Val	Arg																			
																			100															
Asn	Gln	Ile	Ile	Arg	Glu	Leu	Gln	Val	Leu	His	Glu	Cys	Asn	Ser	Pro																			
																			115															
																			130	Val	Gly	Phe	Tyr	Gly	Ala	Phe	Tyr	Ser	Asp	Gly	Glu	Ile	Ser	
																			145				Met	Asp	Gly	Gly	Ser	Leu	Asp	Gln	Val	Leu	Lys	
																			160				150					155					160	
Glu	Ala	Lys	Arg	Ile	Pro	Glu	Asp	Ile	Leu	Gly	Lys	Val	Ser	Ile	Ala																			
																			170															
																			180				Ala	Tyr	Leu	Arg	Glu	Lys	His	Gln	Ile	Met	His	
																			190				165				185					175		
																			200				Pro				190					180		
Arg	Asp	Val	Lys	Pro	Ser	Asn	Ile	Leu	Val	Asn	Ser	Arg	Gly	Glu	Ile																			
																			210															
																			225				Gly	Val	Ser	Gly	Gln	Leu	Ile	Asp	Ser	Met	Ala	
																			240				215				200					205		
																			255				230				220					210		
Leu	Val	Glu	Leu	Ala	Ile	Gly	Arg	Tyr	Pro	Trp	Ser	Pro	Glu	Arg	Leu	Gln																		
																			260															
																			275				Ser	Phe	Gly	Arg	Pro	Val	Val	Asp	Gly	Ala	Asp	
																			290				265				280				285			
																			300				295				280				300			
Ile	Ser	Gly	His	Gly	Met	Asp	Ser	Arg	Pro	Ala	Met	Ala	Ile	Phe	Glu																			
																			310															
																			325				Val	Asn	Glu	Pro	Pro	Pro	Lys	Leu	Pro	Ser	Gly	
																			340				310				330				335			
																			355				325				345				350			
Asn	Pro	Ala	Glu	Arg	Ala	Asp	Leu	Lys	Leu	Leu	Thr	Asn	His	Ala	Phe																			
																			360															
Ile	Lys	Arg	Ser	Glu																														

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
(B) CLONE: 8541070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Met Thr Gly Ser Thr Pro Cys Ser Ser Met Ser Asn His Thr  
1 5 10 15

Lys Glu Arg Val Thr Met Thr Lys Val Thr Leu Glu Asn Phe Tyr Ser  
 20 25 30  
 Asn Leu Ile Ala Gln His Glu Glu Arg Glu Met Arg Gln Lys Lys Leu  
 35 40 45  
 Glu Lys Val Met Glu Glu Glu Gly Leu Lys Asp Glu Glu Lys Arg Leu  
 50 55 60  
 Arg Arg Ser Ala His Ala Arg Lys Glu Thr Glu Phe Leu Arg Leu Lys  
 65 70 75 80  
 Arg Thr Arg Leu Gly Leu Glu Asp Phe Glu Ser Leu Lys Val Ile Gly  
 85 90 95  
 Arg Gly Ala Phe Gly Glu Val Arg Leu Val Gln Lys Lys Asp Thr Gly  
 100 105 110  
  
 His Val Tyr Ala Met Lys Ile Leu Arg Lys Ala Asp Met Leu Glu Lys  
 115 120 125  
 Glu Gln Val Gly His Ile Arg Ala Glu Arg Asp Ile Leu Val Glu Ala  
 130 135 140  
 Asp Ser Leu Trp Val Val Lys Met Phe Tyr Ser Phe Gln Asp Lys Leu  
 145 150 155 160  
 Asn Leu Tyr Leu Ile Met Glu Phe Leu Pro Gly Gly Asp Met Met Thr  
 165 170 175  
 Leu Leu Met Lys Lys Asp Thr Leu Thr Glu Glu Thr Gln Phe Tyr  
 180 185 190  
 Ile Ala Glu Thr Val Leu Ala Ile Asp Ser Ile His Gln Leu Gly Phe  
 195 200 205  
 Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Asp Ser Lys Gly  
 210 215 220  
 His Val Lys Leu Ser Asp Phe Gly Leu Cys Thr Gly Leu Lys Lys Ala  
 225 230 235 240  
 His Arg Thr Glu Phe Tyr Arg Asn Leu Asn His Ser Leu Pro Ser Asp  
 245 250 255  
 Phe Thr Phe Gln Asn Met Asn Ser Lys Arg Lys Ala Glu Thr Trp Lys  
 260 265 270  
 Arg Asn Arg Arg Gln Leu Ala Phe Ser Thr Val Gly Thr Pro Asp Tyr  
 275 280 285  
 Ile Ala Pro Glu Val Phe Met Gln Thr Gly Tyr Asn Lys Leu Cys Asp  
 290 295 300  
 Trp Trp Ser Leu Gly Val Ile Met Tyr Glu Met Leu Ile Gly Tyr Pro  
 305 310 315 320  
 Pro Phe Cys Ser Glu Thr Pro Gln Glu Thr Tyr Lys Lys Val Met Asn  
 325 330 335  
 Trp Lys Glu Thr Leu Thr Phe Pro Pro Glu Val Pro Ile Ser Glu Lys  
 340 345 350  
 Ala Lys Asp Leu Ile Leu Arg Phe Cys Cys Glu Trp Glu His Arg Ile  
 355 360 365  
 Gly Ala Pro Gly Val Glu Glu Ile Lys Ser Asn Ser Phe Phe Glu Gly  
 370 375 380  
 Val Asp Trp Glu His Ile Arg Glu Arg Pro Ala Ala Ile Ser Ile Glu  
 385 390 395 400  
 Ile Lys Ser Ile Asp Asp Thr Ser Asn Phe Asp Glu Phe Pro Glu Ser  
 405 410 415  
 Asp Ile Leu Lys Pro Thr Val Ala Thr Ser Asn His Pro Glu Thr Asp  
 420 425 430  
  
 Tyr Lys Asn Lys Asp Trp Val Phe Ile Asn Tyr Thr Tyr Lys Arg Phe  
 435 440 445  
 Glu Gly Leu Thr Ala Arg Gly Ala Ile Pro Ser Tyr Met Lys Ala Ala  
 450 455 460  
 Lys  
 465

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 790790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Leu Gly Ala Val Glu Gly Pro Arg Trp Lys Gln Ala Glu Asp Ile
 1          5          10          15
Arg Asp Ile Tyr Asp Phe Arg Asp Val Leu Gly Thr Gly Ala Phe Ser
 20          25          30

Glu Val Ile Leu Ala Glu Asp Lys Arg Thr Gln Lys Leu Val Ala Ile
 35          40          45
Lys Cys Ile Ala Lys Glu Ala Leu Glu Gly Lys Glu Gly Ser Met Glu
 50          55          60
Asn Glu Ile Ala Val Leu His Lys Ile Lys His Pro Asn Ile Val Ala
 65          70          75          80
Leu Asp Asp Ile Tyr Glu Ser Gly Gly His Leu Tyr Leu Ile Met Gln
 85          90          95
Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
100          105          110
Tyr Thr Glu Arg Asp Ala Ser Arg Leu Ile Phe Gln Val Leu Asp Ala
115          120          125
Val Lys Tyr Leu His Asp Leu Gly Ile Val His Arg Asp Leu Lys Pro
130          135          140
Glu Asn Leu Leu Tyr Tyr Ser Leu Asp Glu Asp Ser Lys Ile Met Ile
145          150          155          160
Ser Asp Phe Gly Leu Ser Lys Met Glu Asp Pro Gly Ser Val Leu Ser
165          170          175
Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
180          185          190
Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
195          200          205
Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ala
210          215          220
Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro
225          230          235          240
Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg His Leu
245          250          255
Met Glu Lys Asp Pro Glu Lys Arg Phe Thr Cys Glu Gln Ala Leu Gln
260          265          270
His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asp Lys Asn Ile His Gln
275          280          285
Ser Val Ser Glu Gln Ile Lys Lys Asn Phe Ala Lys Ser Lys Trp Lys
290          295          300
Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu Gln
305          310          315          320
Leu Gly Thr Ser Gln Glu Gly Gln Gly Gln Thr Ala Ser His Gly Glu
325          330          335

Leu Leu Thr Pro Val Ala Gly Gly Pro Ala Ala Gly Cys Cys Cys Arg
340          345          350
Asp Cys Cys Val Glu Pro Gly Thr Glu Leu Ser Pro Thr Leu Pro His
355          360          365
Gln Leu
370

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 924921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Ser Thr Ser Ala Thr Asp Thr His His Val Glu Leu Ala Arg Glu Arg
 1          5          10          15
Ser Lys Thr Val Thr Ser Phe Tyr Asn Gln Ser Ala Ile Asp Val Val
 20          25          30
Ala Glu Lys Pro Ser Val Arg Leu Thr Pro Thr Met Met Leu Tyr Ser
 35          40          45

Gly Arg Ser Gln Asp Gly Ser His Leu Leu Lys Ser Gly Arg Tyr Leu
 50          55          60
Gln Gln Glu Leu Pro Val Arg Ile Ala His Arg Ile Lys Gly Phe Arg
 65          70          75          80
Ser Leu Pro Phe Ile Ile Gly Cys Asn Pro Thr Ile Leu His Val His
 85          90          95
Glu Leu Tyr Ile Arg Ala Phe Gln Lys Leu Thr Asp Phe Pro Pro Ile
100          105          110
Lys Asp Gln Ala Asp Glu Ala Gln Tyr Cys Gln Leu Val Arg Gln Leu
115          120          125
Leu Asp Asp His Lys Asp Val Val Thr Leu Leu Ala Glu Gly Leu Arg
130          135          140
Glu Ser Arg Lys His Ile Glu Asp Glu Lys Leu Val Arg Tyr Phe Leu
145          150          155          160
Asp Lys Thr Leu Thr Ser Arg Leu Gly Ile Arg Met Leu Ala Thr His
165          170          175
His Leu Ala Leu His Glu Asp Lys Pro Asp Phe Val Gly Ile Ile Cys
180          185          190
Thr Arg Leu Ser Pro Lys Lys Ile Ile Glu Lys Trp Val Asp Phe Ala
195          200          205
Arg Arg Leu Cys Glu His Lys Tyr Gly Asn Ala Pro Arg Val Arg Ile
210          215          220
Asn Gly His Val Ala Ala Arg Phe Pro Phe Ile Pro Met Pro Leu Asp
225          230          235          240
Tyr Ile Leu Pro Glu Leu Leu Lys Asn Ala Met Arg Ala Thr Met Glu
245          250          255
Ser His Leu Asp Thr Pro Tyr Asn Val Pro Asp Val Val Ile Thr Ile
260          265          270
Ala Asn Asn Asp Val Asp Leu Ile Ile Arg Ile Ser Asp Arg Gly Gly
275          280          285
Gly Ile Ala His Lys Asp Leu Asp Arg Val Met Asp Tyr His Phe Thr
290          295          300
Thr Ala Glu Ala Ser Thr Gln Asp Pro Arg Ile Ser Pro Leu Phe Gly
305          310          315          320
His Leu Asp Met His Ser Gly Gly Gln Ser Gly Pro Met His Gly Phe
325          330          335
Gly Phe Gly Leu Pro Thr Ser Arg Ala Tyr Ala Glu Tyr Leu Gly Gly
340          345          350
Ser Leu Gln Leu Gln Ser Leu Gln Gly Ile Gly Thr Asp Val Tyr Leu
355          360          365
Arg Leu Arg His Ile Asp Gly Arg Glu Glu Ser Phe Arg Ile
370          375          380

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1335856

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Glu Thr Val Ile Ser Ser Asp Ser Ser Pro Ala Val Glu Asn Glu
1      5      10      15
His Pro Gln Glu Thr Pro Glu Ser Asn Asn Ser Val Tyr Thr Ser Phe
20      25      30
Met Lys Ser His Arg Cys Tyr Asp Leu Ile Pro Thr Ser Ser Lys Leu
35      40      45
Val Val Phe Asp Thr Ser Leu Gln Val Lys Lys Ala Phe Phe Ala Leu
50      55      60
Val Thr Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys Lys Gln
65      70      75
Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Asn Ile Leu His
85      90      95
Arg Tyr Tyr Lys Ser Ala Leu Val Gln Ile Tyr Glu Leu Glu Glu His
100     105     110
Lys Ile Glu Thr Trp Arg Glu Val Tyr Leu Gln Asp Ser Phe Lys Pro
115     120     125
Leu Val Cys Ile Ser Pro Asn Ala Ser Leu Phe Asp Ala Val Ser Ser
130     135     140

Leu Ile Arg Asn Lys Ile His Arg Leu Pro Val Ile Asp Pro Glu Ser
145     150     155
Gly Asn Thr Leu Tyr Ile Leu Thr His Lys Arg Ile Leu Lys Phe Leu
165     170     175
Lys Leu Phe Ile Thr Glu Phe Pro Lys Pro Glu Phe Met Ser Lys Ser
180     185     190
Leu Glu Glu Leu Gln Ile Gly Thr Tyr Ala Asn Ile Ala Met Val Arg
195     200     205
Thr Thr Thr Pro Val Tyr Val Ala Leu Gly Ile Phe Val Gln His Arg
210     215     220
Val Ser Ala Leu Pro Val Val Asp Glu Lys Gly Arg Val Val Asp Ile
225     230     235
Tyr Ser Lys Phe Asp Val Ile Asn Leu Ala Ala Glu Lys Thr Tyr Asn
245     250     255
Asn Leu Asp Val Ser Val Thr Lys Ala Leu Gln His Arg Ser His Tyr
260     265     270
Phe Glu Gly Val Leu Lys Cys Tyr Leu His Glu Thr Leu Glu Thr Ile
275     280     285
Ile Asn Arg Leu Val Glu Ala Glu Val His Arg Leu Val Val Val Asp
290     295     300
Glu Asn Asp Val Val Lys Gly Ile Val Ser Leu Ser Asp Ile Leu Gln
305     310     315
Ala Leu Val Leu Thr Gly Gly Glu Lys Lys Pro
325     330

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